

ABSTRACT OF THE DISCLOSURE

A method for screening protein-protein interactions that is rapid, easy and generally applicable to a wide array of such interactions is disclosed. This method, an adaptation and combination of certain existing approaches, the T7 phage display libraries and target epitope arrays made, for example, by simultaneous synthesis overlapping peptides of known sequence. These methods provide for high throughput screening that can identify the particular amino acids or domains or epitopes that are of primary importance in the binding interactions between two protein partners.